Amendments to the Specification:

Please replace the paragraph spanning pages 6 and 7 with the following amended paragraph:

--Figure 12(a) shows the structural basis of sialic acid dependence of the NgR2-MAG interaction. Figure 12A-A'' shows that wild-type NgR2 is expressed on the cell surface of transiently transfected COS-7 cells as shown by anti-NgR2 immunocytochemistry (ICC, see A''). NgR2 supports high affinity binding of MAG-Fc (MAG) but not AP-Nogo66 (Nogo66). Figure 12B-B'' the NgR2-ligand binding domain (LBD = LRRNT+LRR+LRRCT = amino acid residues 1-314) is not sufficient to support high affinity MAG binding. Figure 12C-C''''shows the NgR2-'unique' domain (residues 315-420), when fused to the NgR1-LBD (residues 1-314) is sufficient to support high affinity MAG binding. Figure 12D-D'' shows the NgR2-unique domain, when fused to the NgR3-LBD (residues 1-309) does not support MAG binding. Figure 12E-E''''shows NgR2 sequences (residues 315-327) juxtaposed to the NgR2-LBD are necessary for high affinity MAG binding. Figure 12F-F'''' shows that residues ~~1-353~~ 1-346 of NgR1 fused to NgR2 residues 328-420 are not sufficient to support high affinity MAG binding. Figure 12G-G'' shows that introducing a 13-amino acid NgR2-peptide (Pro315-Ser327) juxtaposed to the NgR1-LBD is sufficient to convert NgR1 into a high affinity MAG binding receptor while maintaining the Nogo66 and OMgp binding capacity (called NgR^{OMN}). Figure 12H'-H''shows that mutating N325E in NgR^{OMN} greatly reduces MAG binding. Figure 12(b) shows the alignment of the NgR1, NgR2, and NgR3 sequences juxtaposed to the LBDs, the SpeI restriction sites used to generate chimeric receptors are indicated. The 13 amino acid NgR2 peptide Pro315-Ser327 is underlined. Amino acid N327 is labeled with an asterisk. Figure 1c shows a quantification of the relative binding affinities of MAG to NgR chimeric receptors depicted in Figure 12a. Binding is normalized to wild-type NgR2 (I) which is defined as 100%. –